28.(new) A method of claim 25, wherein the absolute binding affinity to the known core sequence probe is plotted as affinity *versus* mismatch position, and normalized to the affinity of a perfect complement of the known core sequence probe.

29.(new) A method of claim 28, further comprising determining that the target sequence comprises a mutation versus the known sequence if the pattern formed by the normalized affinity plot of the target sequence does not match the pattern formed by an affinity plot of the perfect complement.

Sub C1

30.(new) A method of claim 25, further comprising determining if the absolute binding affinity of the target sequence to the at least one known core sequence probe is weaker than the absolute binding affinity of the known sequence to the at least one known core sequence probe.

B1 Cont.

31.(new) A method of claim 25, wherein the at least one probe is between about 5 and 100 bases in length.

32.(new) A method of claim 31, wherein the at least one probe is between about 5 and 50 bases in length.

33.(new) A method of claim 32, wherein the at least one probe is between about 8 and 30 bases in length.

34.(new) A method of claim 33, wherein the at least one probe is between about 8 and 15 bases in length.

35.(new) A method of claim 25, wherein the mutation in the target sequence is indicative of a genetic disease.

36.(new) A method of claim 35, wherein the genetic disease is sickle cell anemia.

37.(new) A method of claim 35, wherein the genetic disease is cystic fibrosis.

38.(new) A method of claim 35, wherein the genetic disease is associated with a P-53 mutation.

39.(new) A method of claim 25, wherein the mutation in the target sequence is indicative of a genetic predisposition.

B1 cont.

40.(new) A method of claim 39, wherein the genetic predisposition is associated with a particular HLA Class I or HLA Class II gene.

41.(new) A method of claim 39, wherein the HLA Class II gene is selected from the group consisting of DP, DQ and DR beta.

42.(new) A method of claim 25, wherein detecting a mutation in the target sequence is comprised in a genetic evaluation.

43.(new) A method of claim 42, wherein the genetic evaluation is a forensics evaluation.